



PCT

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/019,368

DATE: 08/05/2005

TIME: 11:04:30

Input Set : A:\pto.da.txt

Output Set: N:\CRF4\08042005\J019368.raw

4 <110> APPLICANT: Dean, Nicholas M.  
5 ISIS PHARMACEUTICALS, INC.  
7 <120> TITLE OF INVENTION: Antisense Oligonucleotide Modulation of Human Protein  
8 Kinase C-delta Expression  
10 <130> FILE REFERENCE: ISPH-0458  
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/019,368  
C--> 12 <141> CURRENT FILING DATE: 2001-11-13  
12 <150> PRIOR APPLICATION NUMBER: 1999-05-18  
W--> 13 <151> PRIOR FILING DATE: US 09/313,930  
15 <160> NUMBER OF SEQ ID NOS: 20  
17 <170> SOFTWARE: PatentIn Ver. 2.0  
19 <210> SEQ ID NO: 1  
20 <211> LENGTH: 2104  
21 <212> TYPE: DNA  
22 <213> ORGANISM: Homo sapiens  
24 <220> FEATURE:  
25 <221> NAME/KEY: CDS  
26 <222> LOCATION: (59)..(2089)  
28 <300> PUBLICATION INFORMATION:  
29 <301> AUTHORS: Aris, J . P.  
30 Basta, P. V.  
31 Holmes, W. D.  
32 Ballas, L. M.  
33 Moomaw, C.  
34 Rankl, N. B.  
35 Blobel, G.  
36 Loomis, C. R.  
37 Burns, D. J.  
38 <302> TITLE: Molecular and biochemical characterization of a  
39 recombinant human PKC-delta family member  
40 <303> JOURNAL: Biochim. Biophys. Acta  
41 <304> VOLUME: 1174  
42 <305> ISSUE: 2  
43 <306> PAGES: 171-181  
44 <307> DATE: 1993-08-19  
45 <308> DATABASE ACCESSION NO: L07860  
46 <309> DATABASE ENTRY DATE: 1993-11-02  
48 <400> SEQUENCE: 1  
49 tgcgcgcgcg acccttggcg cctgccccctg caacggggagc cccactgcag gccccacc 58  
51 atg gcg cgc ttc ctg cgc atc gcc ttc aac tcc tat gag ctg ggc tcc 106  
52 Met Ala Pro Phe Leu Arg Ile Ala Phe Asn Ser Tyr Glu Leu Gly Ser  
53 1 5 10 15  
55 ctg cag gcc gag gac gag gcg aac cag ccc ttc tgt gcc gtg aag atg 154

Does Not Comply  
Corrected Diskette Needed  
(p5.1)

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56	Leu Gln Ala Glu Asp Glu Ala Asn Gln Pro Phe Cys Ala Val Lys Met	
57	20 25 30	
59	aag gag gcg ctc agc aca gag cgt ggg aaa aca ctg gtg cag aag aag	202
60	Lys Glu Ala Leu Ser Thr Glu Arg Gly Lys Thr Leu Val Gln Lys Lys	
61	35 40 45	
63	ccg acc atg tat cct gag tgg aag tgc acg ttc gat gcc cac atc tat	250
64	Pro Thr Met Tyr Pro Glu Trp Lys Ser Thr Phe Asp Ala His Ile Tyr	
65	50 55 60	
67	gag ggg cgc gtc atc cag att gtg cta atg cgg gca gca gag gag cca	298
68	Glu Gly Arg Val Ile Gln Ile Val Leu Met Arg Ala Ala Glu Glu Pro	
69	65 70 75 80	
71	gtg tct gag gtg acc gtg ggt gtg tgc gtg ctg gcc gag cgc tgc aag	346
72	Val Ser Glu Val Thr Val Gly Val Ser Val Leu Ala Glu Arg Cys Lys	
73	85 90 95	
75	aag aac aat ggc aag gct gag ttc tgg ctg gac ctg cag cct cag gcc	394
76	Lys Asn Asn Gly Lys Ala Glu Phe Trp Leu Asp Leu Gln Pro Gln Ala	
77	100 105 110	
79	aag gtg ttg atg tct gtt cag tat ttc ctg gag gac gtg gat tgc aaa	442
80	Lys Val Leu Met Ser Val Gln Tyr Phe Leu Glu Asp Val Asp Cys Lys	
81	115 120 125	
83	caa tct atg cgc agt gag gac gag gcc aag ttc cca acg atg aac cgc	490
84	Gln Ser Met Arg Ser Glu Asp Glu Ala Lys Phe Pro Thr Met Asn Arg	
85	130 135 140	
87	cgc gga gcc atc aaa cag gcc aaa atc cac tac atc aag aac cat gag	538
88	Arg Gly Ala Ile Lys Gln Ala Lys Ile His Tyr Ile Lys Asn His Glu	
89	145 150 155 160	
91	ttt atc gcc acc ttc ttt ggg caa ccc acc ttc tgt tct gtg tgc aaa	586
92	Phe Ile Ala Thr Phe Phe Gly Gln Pro Thr Phe Cys Ser Val Cys Lys	
93	165 170 175	
95	gac ttt gtc tgg ggc ctc aac aag caa ggc tac aaa tgc agg caa tgt	634
96	Asp Phe Val Trp Gly Leu Asn Lys Gln Gly Tyr Lys Cys Arg Gln Cys	
97	180 185 190	
99	aac gct gcc atc cac aag aaa tgc atc gac aag atc atc ggc aga tgc	682
100	Asn Ala Ala Ile His Lys Lys Cys Ile Asp Lys Ile Ile Gly Arg Cys	
101	195 200 205	
103	act ggc acc gcg gcc aac agc cgg gac act ata ttc cag aaa gaa cgc	730
104	Thr Gly Thr Ala Ala Asn Ser Arg Asp Thr Ile Phe Gln Lys Glu Arg	
105	210 215 220	
107	ttc aac atc gac atg ccg cac cgc ttc aag gtt cac aac tac atg agc	778
108	Phe Asn Ile Asp Met Pro His Arg Phe Lys Val His Asn Tyr Met Ser	
109	225 230 235 240	
111	ccc acc ttc tgt gac cac tgc ggc agc ctg ctc tgg gga ctg gtg aag	826
112	Pro Thr Phe Cys Asp His Cys Gly Ser Leu Leu Trp Gly Leu Val Lys	
113	245 250 255	
115	cag gga tta aag tgt gaa gac tgc ggc atg aat gtg cac cat aaa tgc	874
116	Gln Gly Leu Lys Cys Glu Asp Cys Gly Met Asn Val His His Lys Cys	
117	260 265 270	
119	cgg gag aag gtg gcc aac ctc tgc ggc atc aac cag aag ctt ttg gct	922
120	Arg Glu Lys Val Ala Asn Leu Cys Gly Ile Asn Gln Lys Leu Leu Ala	

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121	275	280	285	
123	gag gcc ttg aac caa gtc acc cag aga gcc tcc cgg aga tca gac tca	970		
124	Glu Ala Leu Asn Gln Val Thr Gln Arg Ala Ser Arg Arg Ser Asp Ser			
125	290	295	300	
127	gcc tcc tca gag cct gtt ggg ata tat cag ggt ttc gag aag aag acc	1018		
128	Ala Ser Ser Glu Pro Val Gly Ile Tyr Gln Gly Phe Glu Lys Lys Thr			
129	305	310	315	320
131	gga gtt gct ggg gag gac atg caa gac aac agt ggg acc tac ggc aag	1066		
132	Gly Val Ala Gly Glu Asp Met Gln Asp Asn Ser Gly Thr Tyr Gly Lys			
133	325	330	335	
135	atc tgg gag ggc agc agc aag tgc aac atc aac aac ttc atc ttc cac	1114		
136	Ile Trp Glu Gly Ser Ser Lys Cys Asn Ile Asn Asn Phe Ile Phe His			
137	340	345	350	
139	aag gtc ctg ggc aaa ggc agc ttc ggg aag gtg ctg ctt gga gag ctg	1162		
140	Lys Val Leu Gly Lys Gly Ser Phe Gly Lys Val Leu Leu Gly Glu Leu			
141	355	360	365	
143	aag ggc aga gga gag tac tct gcc atc aag gcc ctc aag aag gat gtg	1210		
144	Lys Gly Arg Gly Glu Tyr Ser Ala Ile Lys Ala Leu Lys Lys Asp Val			
145	370	375	380	
147	gtc ctg atc gac gac gac gtg gag tgc acc atg gtt gag aag cgg gtg	1258		
148	Val Leu Ile Asp Asp Asp Val Glu Cys Thr Met Val Glu Lys Arg Val			
149	385	390	395	400
151	ctg aca ctt gcc gca gag aat ccc ttt ctc acc cac ctc atc tgc acc	1306		
152	Leu Thr Leu Ala Ala Glu Asn Pro Phe Leu Thr His Leu Ile Cys Thr			
153	405	410	415	
155	ttc cag acc aag gac cac ctg ttc ttt gtg atg gag ttc ctc aac ggg	1354		
156	Phe Gln Thr Lys Asp His Leu Phe Phe Val Met Glu Phe Leu Asn Gly			
157	420	425	430	
159	ggg gac ctg atg tac cac atc cag gac aaa ggc cgc ttt gaa ctc tac	1402		
160	Gly Asp Leu Met Tyr His Ile Gln Asp Lys Gly Arg Phe Glu Leu Tyr			
161	435	440	445	
163	cgt gcc acg ttt tat gcc gct gag ata atg tgt gga ctg cag ttt cta	1450		
164	Arg Ala Thr Phe Tyr Ala Ala Glu Ile Met Cys Gly Leu Gln Phe Leu			
165	450	455	460	
167	cac agc aag ggc atc att tac agg gac ctc aaa ctg gac aat gtg ctg	1498		
168	His Ser Lys Gly Ile Ile Tyr Arg Asp Leu Lys Leu Asp Asn Val Leu			
169	465	470	475	480
171	ttg gac cgg gat ggc cac atc aag att gcc gac ttt ggg atg tgc aaa	1546		
172	Leu Asp Arg Asp Gly His Ile Lys Ile Ala Asp Phe Gly Met Cys Lys			
173	485	490	495	
175	gag aac ata ttc ggg gag agc cgg gcc agc acc ttc tgc ggc acc cct	1594		
176	Glu Asn Ile Phe Gly Glu Ser Arg Ala Ser Thr Phe Cys Gly Thr Pro			
177	500	505	510	
179	gac tat atc gcc cct gag atc cta cag ggc ctg aag tac aca ttc tct	1642		
180	Asp Tyr Ile Ala Pro Glu Ile Leu Gln Gly Leu Lys Tyr Thr Phe Ser			
181	515	520	525	
183	gtg gac tgg tgg tct ttc ggg gtc ctt ctg tac gag atg ctc att ggc	1690		
184	Val Asp Trp Trp Ser Phe Gly Val Leu Leu Tyr Glu Met Leu Ile Gly			
185	530	535	540	

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187   cag tcc ccc ttc cat ggt gat gat gag gat gaa ctc ttc gag tcc atc   1738
188   Gln Ser Pro Phe His Gly Asp Asp Glu Asp Glu Leu Phe Glu Ser Ile
189   545                               550                               555                               560
191   cgt gtg gac acg cca cat tat ccc cgc tgg atc acc aag gag tcc aag   1786
192   Arg Val Asp Thr Pro His Tyr Pro Arg Trp Ile Thr Lys Glu Ser Lys
193                                 565                               570                               575
195   gac atc ctg gag aag ctc ttt gaa agg gaa cca acc aag agg ctg gga   1834
196   Asp Ile Leu Glu Lys Leu Phe Glu Arg Glu Pro Thr Lys Arg Leu Gly
197                                 580                               585                               590
199   atg acg gga aac atc aaa atc cac ccc ttc ttc aag acc ata aac tgg   1882
200   Met Thr Gly Asn Ile Lys Ile His Pro Phe Phe Lys Thr Ile Asn Trp
201   595                               600                               605
203   act ctg ctg gaa aag cgg agg ttg gag cca ccc ttc agg ccc aaa gtg   1930
204   Thr Leu Leu Glu Lys Arg Arg Leu Glu Pro Pro Phe Arg Pro Lys Val
205   610                               615                               620
207   aag tca ccc aga gac tac agt aac ttt gac cag gag ttc ctg aac gag   1978
208   Lys Ser Pro Arg Asp Tyr Ser Asn Phe Asp Gln Glu Phe Leu Asn Glu
209   625                               630                               635                               640
211   aag gcg cgc ctc tcc tac agc gac aag aac ctc atc gac tcc atg gac   2026
212   Lys Ala Arg Leu Ser Tyr Ser Asp Lys Asn Leu Ile Asp Ser Met Asp
213                                 645                               650                               655
215   cag tct gca ttc gct ggc ttc tcc ttt gtg aac ccc aaa ttc gag cac   2074
216   Gln Ser Ala Phe Ala Gly Phe Ser Phe Val Asn Pro Lys Phe Glu His
217   660                               665                               670
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220   Leu Leu Glu Asp
221   675
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225 <211> LENGTH: 676
226 <212> TYPE: PRT
227 <213> ORGANISM: Homo sapiens
229 <400> SEQUENCE: 2
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234   20                               25                               30
236   Lys Glu Ala Leu Ser Thr Glu Arg Gly Lys Thr Leu Val Gln Lys Lys
237   35                               40                               45
239   Pro Thr Met Tyr Pro Glu Trp Lys Ser Thr Phe Asp Ala His Ile Tyr
240   50                               55                               60
242   Glu Gly Arg Val Ile Gln Ile Val Leu Met Arg Ala Ala Glu Glu Pro
243   65                               70                               75                               80
245   Val Ser Glu Val Thr Val Gly Val Ser Val Leu Ala Glu Arg Cys Lys
246   85                               90                               95
248   Lys Asn Asn Gly Lys Ala Glu Phe Trp Leu Asp Leu Gln Pro Gln Ala
249   100                               105                               110
251   Lys Val Leu Met Ser Val Gln Tyr Phe Leu Glu Asp Val Asp Cys Lys
252   115                               120                               125
254   Gln Ser Met Arg Ser Glu Asp Glu Ala Lys Phe Pro Thr Met Asn Arg

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255	130	135	140
257	Arg Gly Ala Ile Lys Gln Ala Lys Ile His Tyr Ile Lys Asn His Glu		
258	145	150	155
260	Phe Ile Ala Thr Phe Phe Gly Gln Pro Thr Phe Cys Ser Val Cys Lys		
261	165	170	175
263	Asp Phe Val Trp Gly Leu Asn Lys Gln Gly Tyr Lys Cys Arg Gln Cys		
264	180	185	190
266	Asn Ala Ala Ile His Lys Lys Cys Ile Asp Lys Ile Ile Gly Arg Cys		
267	195	200	205
269	Thr Gly Thr Ala Ala Asn Ser Arg Asp Thr Ile Phe Gln Lys Glu Arg		
270	210	215	220
272	Phe Asn Ile Asp Met Pro His Arg Phe Lys Val His Asn Tyr Met Ser		
273	225	230	235
275	Pro Thr Phe Cys Asp His Cys Gly Ser Leu Leu Trp Gly Leu Val Lys		
276	245	250	255
278	Gln Gly Leu Lys Cys Glu Asp Cys Gly Met Asn Val His His Lys Cys		
279	260	265	270
281	Arg Glu Lys Val Ala Asn Leu Cys Gly Ile Asn Gln Lys Leu Leu Ala		
282	275	280	285
284	Glu Ala Leu Asn Gln Val Thr Gln Arg Ala Ser Arg Arg Ser Asp Ser		
285	290	295	300
287	Ala Ser Ser Glu Pro Val Gly Ile Tyr Gln Gly Phe Glu Lys Lys Thr		
288	305	310	315
290	Gly Val Ala Gly Glu Asp Met Gln Asp Asn Ser Gly Thr Tyr Gly Lys		
291	325	330	335
293	Ile Trp Glu Gly Ser Ser Lys Cys Asn Ile Asn Asn Phe Ile Phe His		
294	340	345	350
296	Lys Val Leu Gly Lys Gly Ser Phe Gly Lys Val Leu Leu Gly Glu Leu		
297	355	360	365
299	Lys Gly Arg Gly Glu Tyr Ser Ala Ile Lys Ala Leu Lys Lys Asp Val		
300	370	375	380
302	Val Leu Ile Asp Asp Asp Val Glu Cys Thr Met Val Glu Lys Arg Val		
303	385	390	395
305	Leu Thr Leu Ala Ala Glu Asn Pro Phe Leu Thr His Leu Ile Cys Thr		
306	405	410	415
308	Phe Gln Thr Lys Asp His Leu Phe Phe Val Met Glu Phe Leu Asn Gly		
309	420	425	430
311	Gly Asp Leu Met Tyr His Ile Gln Asp Lys Gly Arg Phe Glu Leu Tyr		
312	435	440	445
314	Arg Ala Thr Phe Tyr Ala Ala Glu Ile Met Cys Gly Leu Gln Phe Leu		
315	450	455	460
317	His Ser Lys Gly Ile Ile Tyr Arg Asp Leu Lys Leu Asp Asn Val Leu		
318	465	470	475
320	Leu Asp Arg Asp Gly His Ile Lys Ile Ala Asp Phe Gly Met Cys Lys		
321	485	490	495
323	Glu Asn Ile Phe Gly Glu Ser Arg Ala Ser Thr Phe Cys Gly Thr Pro		
324	500	505	510
326	Asp Tyr Ile Ala Pro Glu Ile Leu Gln Gly Leu Lys Tyr Thr Phe Ser		
327	515	520	525

VERIFICATION SUMMARY

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Input Set : A:\pto.da.txt

Output Set: N:\CRF4\08042005\J019368.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:13 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD